OK to enter K.Kerr 10/6/03

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 7, line 7, with the following rewritten paragraph:

SEQ ID NO: 44 is the nucleotide sequence of the full-length ~~acyltransacylase~~ O-acetyl transferase clone TAX6.

Please replace the paragraph beginning at page 7, line 9, with the following rewritten paragraph:

SEQ ID NO: 45 is the deduced amino acid sequence of the full-length ~~acyltransacylase~~ O-acetyl transferase clone TAX6.

Please replace the paragraph beginning at page 33, line 9, with the following rewritten paragraph:

~~An additional transacylase~~Another cDNA clone, TAX6 (SEQ ID NO: 44), was identified by using 40 ng of radio-labeled Probe 6 (SEQ ID NO: 11) to screen the *T. cuspidata* library. This full-length clone was 99% identical to Probe 6 (SEQ ID NO: 11) and 99% identical to the deduced amino acid sequence of Probe 6 (SEQ ID NO: 12), indicating that the probe had located its cognate.

Please replace the Abstract on page 57 with the following rewritten Abstract:

Transacylase enzymes of *Taxus cuspidata* and the use of such enzymes to produce Taxol™, related taxoids, as well as intermediates in the Taxol™ biosynthetic pathway are disclosed. Examples of specific enzymes described herein include taxadienol 5-O-acetyl transacylase (TAX1) and 10-deacetylbaccatin III-10-O-acetyl transferase (TAX6). Also disclosed are nucleic acid sequences encoding the *T. cuspidata* transacylase enzymes. ~~Specific non-limiting embodiments include nucleic acid sequences encoding 10-deacetylbaccatin III-10-O-acetyl transferase.~~

SEQ ID NO: 40 is an amino acid sequence variant that allowed for the design of the AT-FOR4 PCR primer.

SEQ ID NO: 41 is a consensus amino acid sequence that allowed for the design of the AT-REV1 PCR primer.

SEQ ID NO: 42 is a PCR primer, useful for identifying transacylases.

SEQ ID NO: 43 is a PCR primer, useful for identifying transacylases.

SEQ ID NO: 44 is the nucleotide sequence of the full-length acyltransacylase clone TAX6.

SEQ ID NO: 45 is the deduced amino acid sequence of the full-length acyltransacylase clone TAX6.

SEQ ID NO: 46 is a PCR primer, useful for identifying TAX6.

SEQ ID NO: 47 is a PCR primer, useful for identifying TAX6.

SEQ ID NO: 48 is a 6-amino acid motif commonly found in transacylases.

SEQ ID NO: 49 is the nucleotide sequence of the full-length acyltransacylase clone TAX5.

SEQ ID NO: 50 is the deduced amino acid sequence of the full-length acyltransacylase clone TAX5.

SEQ ID NO: 51 is the nucleotide sequence of the full-length acyltransacylase clone TAX7.

SEQ ID NO: 52 is the deduced amino acid sequence of the full-length acyltransacylase clone TAX7.

SEQ ID NO: 53 is the nucleotide sequence of the full-length acyltransacylase clone TAX10.

SEQ ID NO: 54 is the deduced amino acid sequence of the full-length acyltransacylase clone TAX10.

SEQ ID NO: 55 is the nucleotide sequence of the full-length acyltransacylase clone TAX12.

SEQ ID NO: 56 is the deduced amino acid sequence of the full-length acyltransacylase clone TAX12.

SEQ ID NO: 57 is the nucleotide sequence of the full-length acyltransacylase clone TAX13.

Correction to Amendment C 4/25/03

and double bond rearrangement to form taxa-4(2), 11(12)-dien-5α-ol, followed by acetylation to taxa-4(20),11(12)-dien-5α-yl acetate. The acetate is further converted to 10-deacetylbaccatin III, baccatin III, and Taxol™. In the figure, "a" denotes the activities of taxadiene synthase and taxadiene-5α-hydroxylase (in that order); "b" denotes taxadien-5α-ol acetyl transacylase; and "c" – "e" denote several subsequent steps.

C8

Please replace the paragraph at page 9, lines 1-18 with the following:

Figures 5A-5G

~~**Figure 5**~~ shows data obtained from a coupled gas chromatographic-mass spectrometric (GC-MS) analysis of the biosynthetic taxadien-5α-yl acetate formed during the incubation of taxadien-5α-ol with soluble enzyme extracts from isopropyl β-D-thiogalactoside (IPTG)-induced *E. coli* JM109 cells transformed with full-length acyltransferase clones TAX1 and TAX2. Panels **A** and **B** show the respective GC and MS profiles of authentic taxadien-5α-ol; panels **C** and **D** show the respective GC and MS profiles of authentic taxadien-5α-yl acetate; panel **E** shows the GC profile of taxadien-5α-ol (11.16 minutes), taxadien-5α-yl acetate (11.82 minutes), dehydrated taxadien-5α-ol ("TOH-H_2O" peak), and a contaminant, bis-(2-ethylhexyl)phthlate ("BEHP" peak, a plasticizer, CAS 117-81-7, extracted from buffer) after incubation of taxadien-5α-ol and acetyl coenzyme A with the soluble enzyme fraction derived from *E. coli* JM109 transformed with the full-length clone TAX1. Panel **F** shows the mass spectrum of biosynthetically formed taxadien-5α-yl acetate by the recombinant enzyme (11.82 minute peak in GC profile Panel E); panel **G** shows the GC profile of the products generated from taxadien-5α-ol and acetyl coenzyme A by incubation with the soluble enzyme fraction derived from *E. coli* JM109 cells transformed with the full-length clone TAX2 (note the absence of taxadien-5α-yl acetate indicating that this clone is inactive in the transacylase reaction).

C9

KK 10/7/03

Please replace the paragraph at page 15, lines 9-16 with the following:

The National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST™, Altschul et al.. *J. Mol. Biol.* **215**:403-410, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence-analysis programs blastp, blastn, blastx, tblastn and tblastx. BLAST™ can be accessed at the NCBI online site under the

C10